

Regulation of inflorescence architecture

Sarah Hake₁, Volker Brendel₂, Dave Jackson₃, Toby Kellogg₄, Rob Martienssen₃, Torbert Rocheford₅ and Bob Schmidt₆

Plant Gene Expression Center, Albany CA
University of Illinois, Urbana/Champaign, IL
Cold Spring Harbor, NY
University of Missouri, St. Louis

Generating new mutants

Working with Dr. Gerry Neuffer, we have produced and screened EMS mutants for the second summer in a row. The first summer we screened B73 and B73/Mo17 F2 populations. This summer we screened EMS mutagenized A619. We also screened a small population of Mo17. The list of mutants and pictures have gone to MaizeGDB. Below are a few pictures from this summer. B73 mutagenized material is shared with Cliff Weil's project on tilling.



barren inflorescence

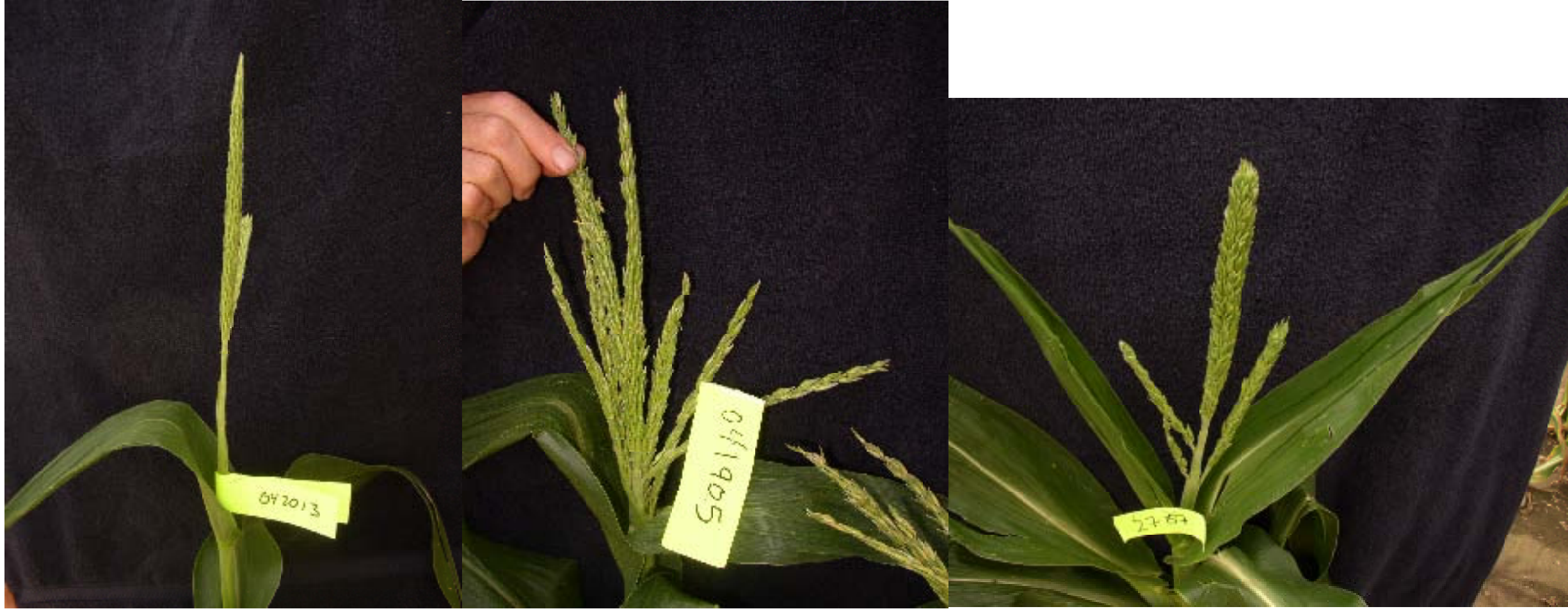
mild tassel seed

tassel sheath



normal compared to narrow leaf

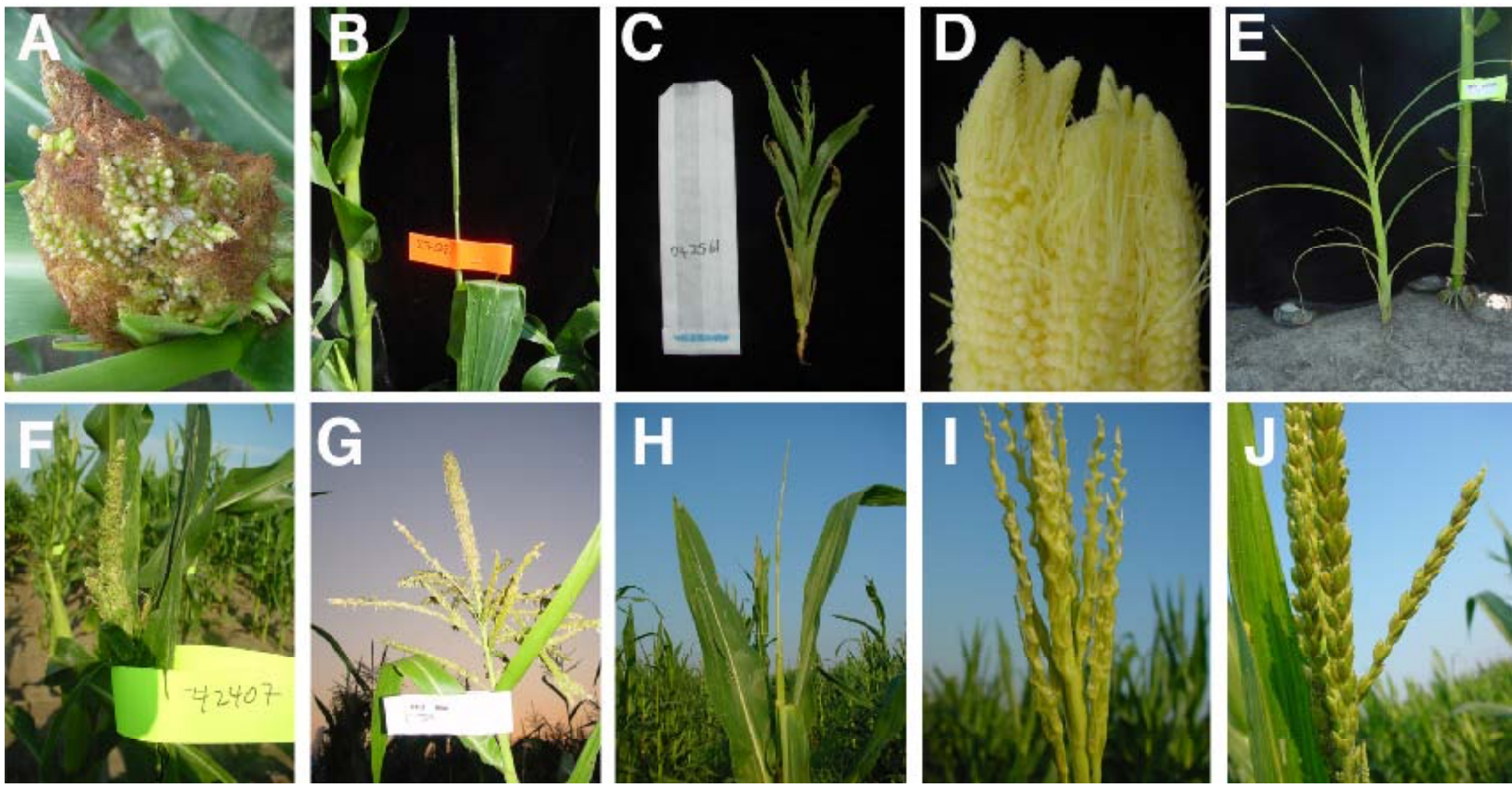
severe tassel seed



less branched tassel

Fasciated main rachis

thick tassel dwarf



A) tassel seed, B) unbranched, C) miniature, D) fasciated, E) needle leaves, F) adherent, G) fat tassel, H) barren, I) no spikelets, J) rounded spikelets

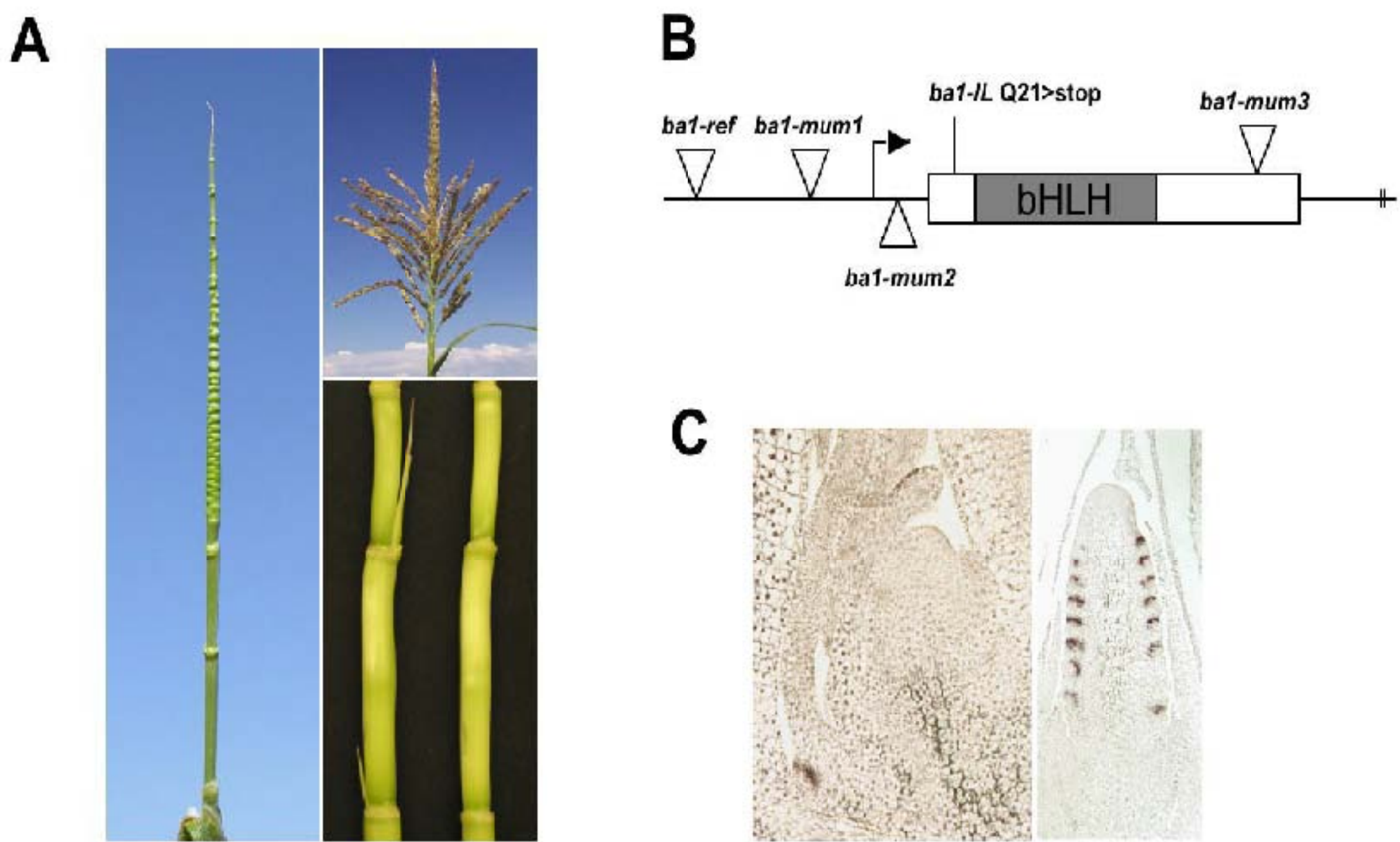


scoring tassels before the storm

setting up crosses

Isolation and analysis of barren stalk1

The ba1 gene was cloned in the Schmidt lab and shown to be expressed in distinct zones in the inflorescence. A) mutant phenotype. B) insertion alleles. C) in situ expression pattern.



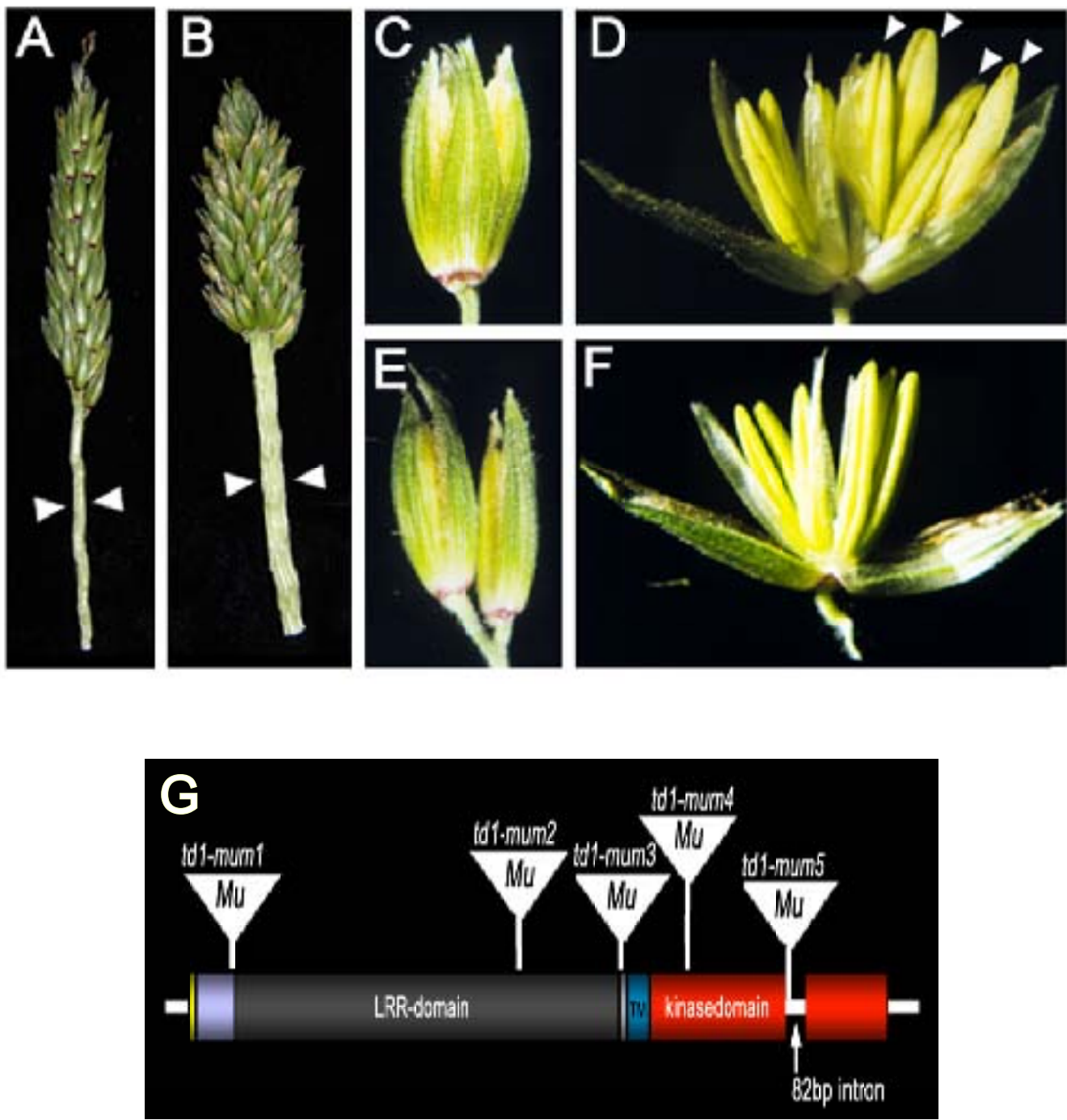
Mapping QTL to known mutants

The Rocheford lab is mapping QTL that regulate inflorescence architecture.

Inflorescence Mutants and QTL associations			
** NOTE ** There are QTLs in bins not listed in this table (to my knowledge, no identified mutant loci in these bins)			
Mutant	Name	Bin	QTL associations (traits)
c22	compact plant2	0.01	
ifa1	indeterminate floral apex1	1.02-1.03	
qcobd5	QTL cob diameter5	1.02	
qcobd11	QTL cob diameter11	1.02 side spike	
qcobd27	QTL cob diameter27	1.02 side spike	
qcobd32	QTL cob diameter32	1.02 side spike	
ts2	tassel seed2	1.03	
qcobd23	QTL cob diameter23	1.03	
	CQRAV28R (clavata1-like gene from pioneer)		
civ28		1.03	
qcobd33	QTL cob diameter33	1.06	branch #, total spikelets, total meristems, total spikelets/branch #, Branch
bif2	barren inflorescence2	1.06	1.06 #L2, L3/L1, L2/L1
qcobd6	QTL cob diameter6	1.07	L2, branch #, L3/L2, L3/L1, 1.07 L2/L1
qcobd12	QTL cob diameter12	1.07	L2, branch #, L3/L2, L3/L1, 1.07 L2/L1
qcobd24	QTL cob diameter24	1.07	L2, branch #, L3/L2, L3/L1, 1.07 L2/L1
qcobd28	QTL cob diameter28	1.07	L2, branch #, L3/L2, L3/L1, 1.07 L2/L1
ad1	adherent1	1.08	Branch #, side spike
an1	anther ear1	1.08	Branch #, side spike
id1	indeterminate1	1.08	Branch #, side spike
ts3	tassel seed3	1.09	
ts1	tasselless1	1.09	
kp	bell-like gene interacts with KN1	1.09	
kn1	knotted1	1.10	
knx8	knotted related homeobox8	1.10	
ts6	tassel seed6	1.11	side spike
ids1	indeterminate spikelet1	1.11	side spike
qcobd13	QTL cob diameter13	1.12	
qcobd14	QTL cob diameter14	1.12	branch #, side spike, total
lfyB	leafyB (Doebley)	2.03	2.03 seed row number (doebley)
ts1	tassel seed1	2.04	L3, branch #, angle, side spike, 2.04 L3/L2
ba2	barren stalk2	2.04	L3, branch #, angle, side spike, 2.04 L3/L2
cent1B	centroradialis-like gene - McSteen	2.04	L3, branch #, angle, side spike, 2.04 L3/L2
abp1	abp1	2.04	
qcobd15	QTL cob diameter15	2.06	L2, total spikelets, total meristems, total spikelets/branch #, branch#L2, 2.06 L3/L2, L3/L1, L2/L1
qcobd7	QTL cob diameter7	2.07	angle, total spikelets/branch#
qcobd25	QTL cob diameter25	2.07	angle, total spikelets/branch#
qcobd29	QTL cob diameter29	2.07	angle, total spikelets/branch#
qcobd34	QTL cob diameter34	2.07	angle, total spikelets/branch#
qcobd16	QTL cob diameter16	2.08	main spike, side spike, total
pinA	CBSA021 pinformed-like gene Pioneer	2.09	meristems
knx4	knotted related homeobox4	2.10	L2, total spikelets/branch#
ra2	ramosa2	3.02	branch #, total spikelets/branch#
zag4	Zea AGAMOUS homologue4-transcription factor	3.02	branch #, total spikelets/branch#
tp3	teopod3	3.03	L1, branch #, total spikelets/branch#
ts4	tassel seed4	3.04	L3, L3/L1, L2/L1
tru1	tassels replace upper ears1	3.04	L3, L3/L1, L2/L1
qcobd1	QTL cob diameter1	3.04	L3, L3/L1, L2/L1
o15	liguleless3	3.04	L3, L3/L1, L2/L1
fea3	fasciated ear3	3.04	
te1	terminal ear1	3.05	L2, L3, branch #, branch#L2, 3.05 L3/L2, L3/L1, L2/L1
zag2	Zea AGAMOUS homologue2- expression in female inflorescence	3.05	L2, L3, branch #, branch#L2, 3.05 L3/L2, L3/L1, L2/L1
ub1	unbranched1 (may be identical to lg2)	3.06	angle
erf4a	ERF gene in tassels/ears Magnani	3.06	
lg2	liguleless2	3.06	angle
ba1	barren stalk1	3.06	angle
pinB	CBSA021 pinformed-like gene Pioneer	4.01	main spike, total
ra3	ramosa3	4.01	main spike, total
sos1	suppressor of sessile spikelets1	4.02	
ps1	paired rows1	4.02	
ts5	tassel seed5	4.03	
qcobd8	QTL cob diameter8	4.05	
fea2	fasciated ear2	4.05	
qcobd17	QTL cob diameter17	4.06	side spike
tu1	tunicate1	4.07	
qcobd2	QTL cob diameter2	4.07	
mpA	CFRME33monopterous-like gene Pioneer	4.08	branch#, main spike, total
qcobd18	QTL cob diameter18	5.00	spikelets, total meristems, total spikelets/branch#, branch#L2, 5.00-5.01
fea1	fasciated ear1	5.00	
chw40	CCRBA40R clavata1-like gene Pioneer	5.01	
qcobd19	QTL cob diameter19	5.03	angle, side spike
mpB	CFRME33monopterous-like gene Pioneer	5.03	angle, side spike
td1	thick tassel dwarf1	5.04	L2, side spike
qcobd9	QTL cob diameter9	5.04	L2, side spike
qcobd3	QTL cob diameter3	5.05	main spike, total spikelets, total
pt	polytypic-McClintock (bearded ear)	5.06	meristems
si1	silky1	6.02	L3/L2, L3/L1, L2/L1
zag1	Zea AGAMOUS homologue1- strong expression in female	6.05	branch#L2
pt1	polytypic ear1	6.06	
rs1	rough sheath1	7.00	side spike, branch#L2
civ64	CRWAX64R clavata1-like gene Pioneer	7.01	
ra1	ramosa1	7.02	branch #, branch#L2
tp1	teopod1	7.03	L1, L2, Branch#L2
qcobd10	QTL cob diameter10	7.03	L1, L2, Branch#L2
qcobd20	QTL cob diameter20	7.03	L1, L2, Branch#L2
qcobd26	QTL cob diameter26	7.03	L1, L2, Branch#L2
qcobd30	QTL cob diameter30	7.03	L1, L2, Branch#L2
qcobd35	QTL cob diameter35	7.03	L1, L2, Branch#L2
ra3	ramosa3	7.04	
o15	opaque endosperm15 (ear in tassel) may be identical to gzt1	7.05	branch#
bd1	branched silkless1	7.06	
bf1	barren inflorescence1	8.00	
zmm2	Zea mays MADS2	8.02	
ap21	??	8.03	
clt1	clumped tassel1	8.04	
p22	paired rows2	8.04	
knx5	knotted related homeobox5	8.05	branch#, branch#L2
qcobd31	QTL cob diameter31	8.07	
qcobd36	QTL cob diameter36	8.07	
qcobd21	QTL cob diameter21	8.08	L2, branch#
ba1	barren stalk fastigiate1	9.00	side spike
qcobd4	QTL cob diameter4	9.01	side spike
fas1	fasciated ear1	9.05	L2
pinC	CBSA021 pinformed-like gene Pioneer	9.05	
cr4	crinkly4	10.02	
cen2	CERA94 centroradialis gene - Pioneer	10.02	
tp2	teopod2	10.04	branch #, side spike
qcobd22	QTL cob diameter22	10.04	branch #, side spike
cen1A	centroradialis-like gene McSteen	10.04	
ra2-like1	ra2 like gene	10.10	side spike

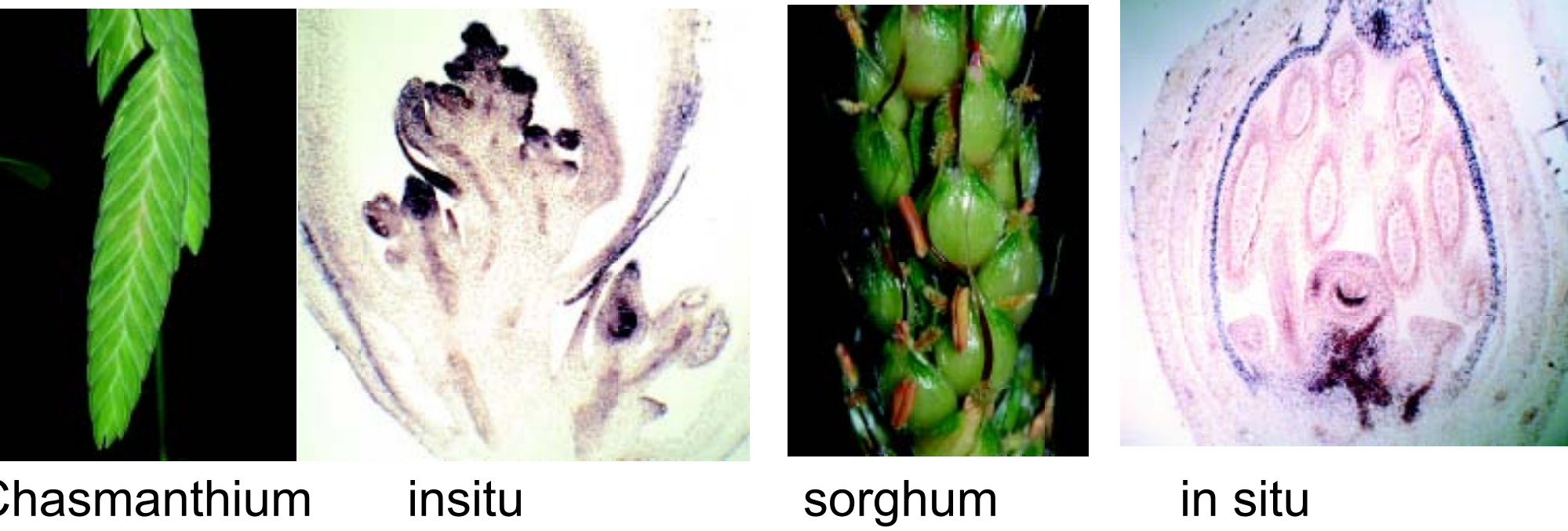
Isolation and analysis of thick tassel dwarf

In collaboration with Peter Bommert and Wolfgang Werr, the Hake lab has shown that thick tassel dwarf is a clavata1 ortholog. A) normal tassel rachis, B) td1 rachis, C) td1 spikelet, D) td1 florets with extra spikelets, E) normal florets, G) position of insertion



Evolutionary studies

The Kellogg lab has carried out in situ in different grasses that span the major diversification of the family using the MADS box gene, leafy hull sterile. In sorghum, maize, millet and rice, which have florets that mature from top to bottom (basipetally) in the spikelet, LHS1 is expressed only in the upper floret. In contrast, LHS1 is expressed in several florets of the spikelets of Chasmanthium which have florets that develop from bottom to top (acropetally).



Comparative studies

The Rocheford lab is examining the tassel morphology of 100 diverse inbreds in collaboration with Ed Buckler. The inbreds are being sequenced by his group to determine whether polymorphisms in any of the inflorescence genes we are studying correlate with variation in morphology. Below are examples of tassel morphology variation found in these inbreds.

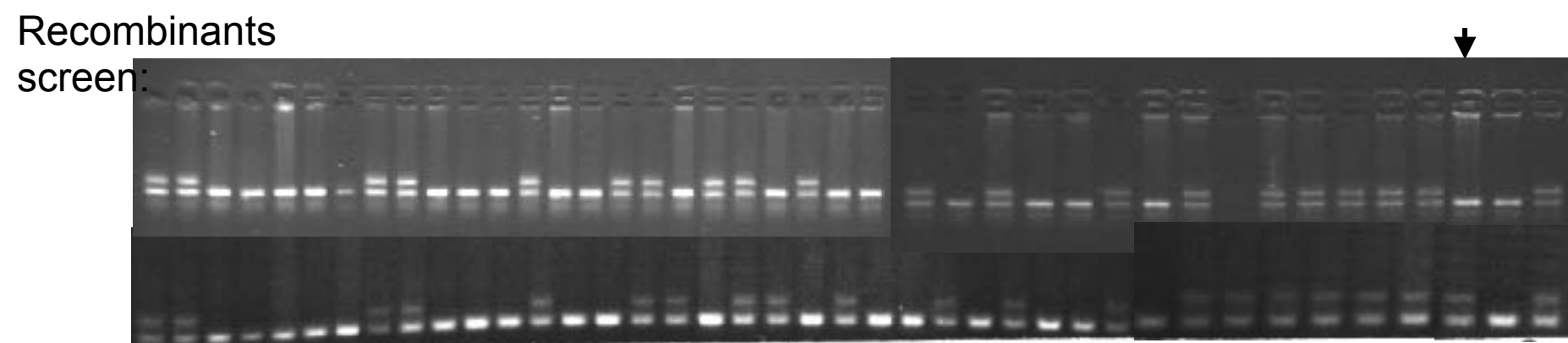


Positional cloning

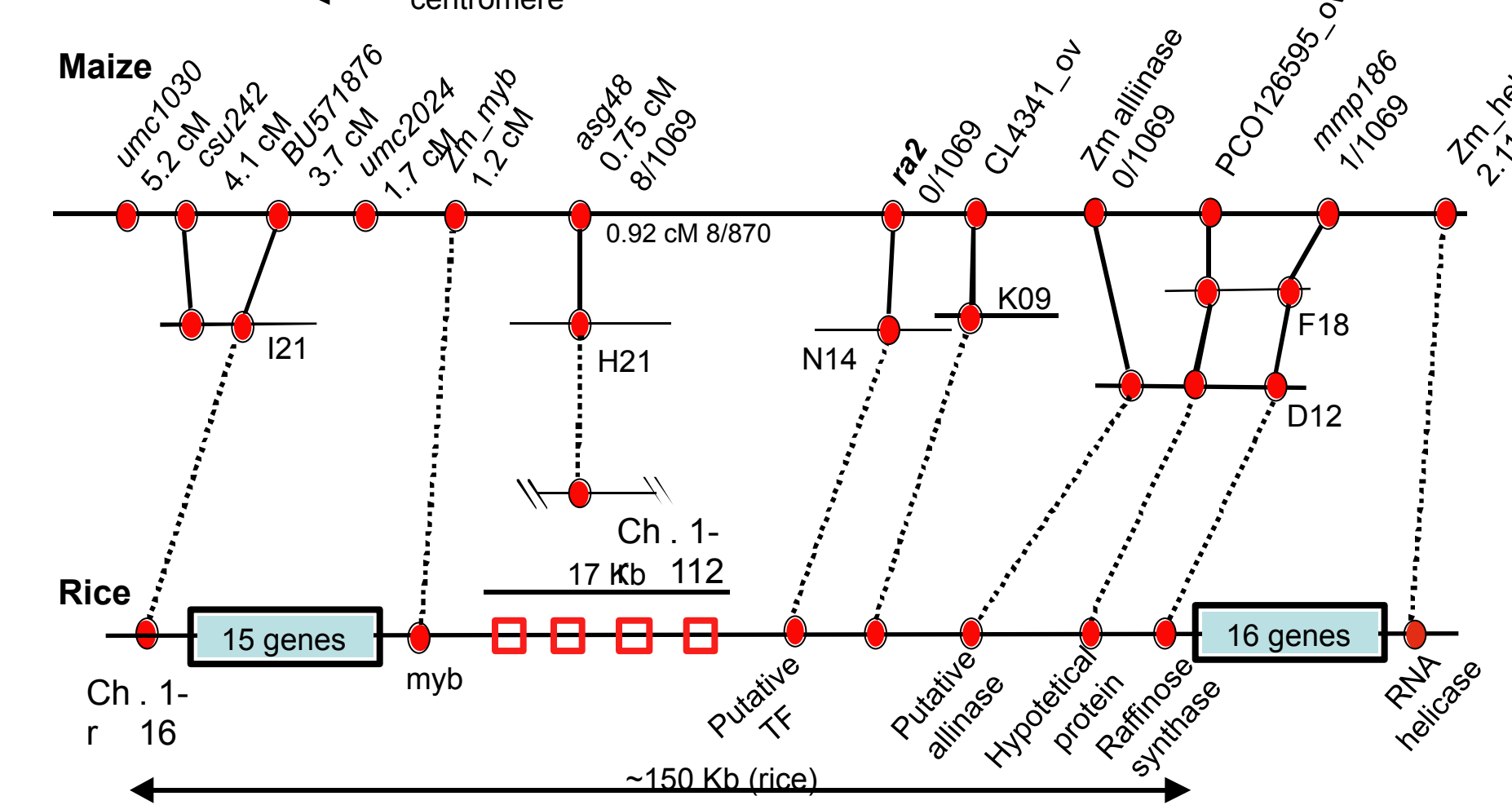
The Hake and Jackson labs have successfully walked to the ramosa2 and ramosa3 genes in maize and are very close to tasselseed4.



Below we present an example of the PCR screen for recombinants and the alignment of the region of synteny between rice and maize for the region around ra2 and for ts4.



Grow the recombinants, score phenotype (ra2) with other marker- perform BAC-markers detection to link physical and genetic maps



A comparison between the genetic (top), and physical (middle) maps of maize corresponding to the ra2 region and the orthologous region in chromosome 1 of rice. The area boxed in blue is non-syntentic between maize and rice. Rice asg48 is on chromosome 1 but unlinked to rmp186. There are four hypothetical protein ORFs (empty boxes) between the rice myb and LDB genes for which there are no significantly similar ze sequences. Solid lines represent BAC-marker correspondence by PCR and/or Southern. Broken lines represent matches obtained by BLAST in various databases. MaizeBACs are represented by their last three address numbers. Not drawn to proportion but the number and order of rice genes follow their annotation in GenBank.

Maize vs Rice Physical Map in region of ts4

